

11420122.APP
SEQUENCE LISTING

<110> Pausch, Mark H
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011

<141> 1997-03-11

<150> 07/332,312

<151> 1994-10-31

<150> PCT/US95/14364

<151> 1995-10-25

<160> 67

<170> PatentIn Ver. 2.1

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 35 40 45
 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
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 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
 65 70 75 80
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 225 230 235 240
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 290 295 300
 Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
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| atattgtttct | ccttgcttgg | aatacctcta | acactgggta | ccatcgctga | cttggcaggt | 240 |
| aaattcctat | ctgaacatct | tgtttggttg | tatggaaact | atttgaaatt | aaaatatctc | 300 |
| atattgtcac | gacatcgaaa | agaacggaga | gagcacgttt | gtgagcactg | tcacagtcac | 360 |
| ggaatggggc | atgatatgaa | tatcgaggag | aaaagaattc | ctgcattcct | ggtattagct | 420 |
| attctgatag | tatatacagc | gtttggcggt | gtcctaattg | caaaattaga | gccgtggtct | 480 |
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65 70 75 80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
100 105 110

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135

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165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
210 215 220

Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
225 230 235 240

Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
245 250 255

Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
260 265 270

Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
275 280 285

Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
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 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
 50 55 60
 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
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| Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr | 165 | | 170 | 175 |
| Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro | 180 | | 185 | 190 |
| Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser | 195 | 200 | | 205 |
| Leu Tyr Tyr Ser Tyr Val Thr Ile Thr Thr Ile Gly Phe Gly Asp Tyr | 210 | 215 | 220 | |
| Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe | 225 | 230 | 235 | 240 |
| Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly | 245 | | 250 | 255 |
| Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys | 260 | 265 | | 270 |
| Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr | 275 | 280 | 285 | |
| Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg | 290 | 295 | 300 | |
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| Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg | 340 | 345 | | 350 |
| Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly | 355 | 360 | 365 | |
| Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu | 370 | 375 | 380 | |
| Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu | 385 | 390 | 395 | 400 |
| Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu | 405 | | 410 | 415 |
| Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser | 420 | 425 | | 430 |
| Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr | 435 | 440 | 445 | |
| Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu | | | | |

450

455

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Trp

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<213> Caenorhabditis elegans

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<223> X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

<400> 38
Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
1 5 10 15
Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
20 25 30
Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
35 40 45
Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
50 55 60
Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly
65 70 75 80
Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
85 90 95
Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
100 105 110
Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
115 120 125
Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
130 135 140
Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
145 150 155 160
Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
165 170 175
Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
180 185 190
Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
195 200 205
Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
210 215 220
Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln

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| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| 225 | | 230 | | 235 | | 240 |
| Asp | Ala | Arg | Ser | Ala | Leu | Ala |
| | | | | 245 | Val | Val |
| | | | | 250 | Gly | Gly |
| | | | | | Lys | Val |
| | | | | | Val | Val |
| | | | | | Leu | Val |
| | | | | | 255 | |
| Ser | Glu | Leu | Tyr | Ala | Asn | Leu |
| | | | | 260 | Met | Gln |
| | | | | | 265 | Lys |
| | | | | | Arg | Ala |
| | | | | | Arg | Asn |
| | | | | | Met | Ser |
| | | | | | 270 | |
| Arg | Glu | Ala | Phe | Ile | Val | Glu |
| | | | | | | 280 |
| | | | | | | Asn |
| | | | | | | Leu |
| | | | | | | Tyr |
| | | | | | | Val |
| | | | | | | Ser |
| | | | | | | 285 |
| | | | | | | Lys |
| | | | | | | His |
| | | | | | | Ile |
| | | | | | | Ile |
| Pro | Phe | Ile | Pro | Thr | Asp | Ile |
| | | | | | | 290 |
| | | | | | | Arg |
| | | | | | | Cys |
| | | | | | | Ile |
| | | | | | | Arg |
| | | | | | | Tyr |
| | | | | | | 300 |
| | | | | | | Ile |
| | | | | | | Asp |
| | | | | | | Gln |
| | | | | | | Thr |
| Ala | Asp | Ala | Ala | Thr | Ile | Ser |
| | | | | | | 310 |
| | | | | | | Thr |
| | | | | | | Ser |
| | | | | | | Ser |
| | | | | | | 315 |
| | | | | | | Ala |
| | | | | | | Ile |
| | | | | | | Asp |
| | | | | | | Met |
| | | | | | | Gln |
| | | | | | | 320 |
| Ser | Cys | Arg | Phe | Cys | His | Ser |
| | | | | | | 325 |
| | | | | | | Arg |
| | | | | | | Tyr |
| | | | | | | Ser |
| | | | | | | 330 |
| | | | | | | Leu |
| | | | | | | Asn |
| | | | | | | Arg |
| | | | | | | Ala |
| | | | | | | Phe |
| | | | | | | 335 |
| | | | | | | Lys |

Xaa

<210> 39
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DEGENERATE
 PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<220>
 <221> variation
 <222> (2)
 <223> N AT BASE 2 INDICATES ANY NUCLEOTIDE

<400> 39
 tnggatwygg wgaywyt 17

<210> 40
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DEGENERATE
 PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40
 rtcwccrwah ccdydggt 18

<210> 41
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 41
 cgcaggcaga gccacaaaga gtacacag 28

<210> 42
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 42
 ggagatcagc taggcacat atttgg 26

<210> 43
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 43
 atgctgcatg cctcatgctt cccagc 26

<210> 44
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 44
 gggtatttaa agagagggct 20

<210> 45
 <211> 426
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val
 1 5 10 15
 Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys
 20 25 30
 Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val
 35 40 45
 Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr
 50 55 60
 Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe
 65 70 75 80
 Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val
 85 90 95
 Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr
 100 105 110
 Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly
 115 120 125
 Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu
 130 135 140
 Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe
 145 150 155 160

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Ile | Ser | Pro | Arg | Thr | Glu | Gly | Gly | Lys | Ile | Phe | Cys | Ile | Ile |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Tyr | Ala | Leu | Leu | Gly | Ile | Pro | Leu | Phe | Gly | Phe | Leu | Leu | Ala | Gly | Val |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gly | Asp | Gln | Leu | Gly | Thr | Ile | Phe | Gly | Lys | Gly | Ile | Ala | Lys | Val | Glu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Asp | Thr | Phe | Ile | Lys | Trp | Asn | Val | Ser | Gln | Thr | Lys | Ile | Arg | Ile | Ile |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ser | Thr | Ile | Ile | Phe | Ile | Leu | Phe | Gly | Cys | Val | Leu | Phe | Val | Ala | Leu |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 |
| Pro | Ala | Ile | Ile | Phe | Lys | His | Ile | Glu | Gly | Trp | Ser | Ala | Leu | Asp | Ala |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Tyr | Phe | Val | Val | Ile | Thr | Leu | Thr | Thr | Ile | Gly | Phe | Gly | Asp | Tyr |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Val | Ala | Gly | Gly | Ser | Asp | Ile | Glu | Tyr | Leu | Asp | Phe | Tyr | Lys | Pro | Val |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Val | Trp | Phe | Trp | Ile | Leu | Val | Gly | Leu | Ala | Tyr | Phe | Ala | Ala | Val | Leu |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ser | Met | Ile | Gly | Arg | Leu | Val | Arg | Val | Ile | Ser | Lys | Lys | Thr | Lys | Glu |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 |
| Glu | Val | Gly | Glu | Phe | Arg | Ala | His | Ala | Ala | Glu | Trp | Thr | Ala | Asn | Val |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Thr | Ala | Glu | Phe | Lys | Glu | Thr | Arg | Arg | Arg | Leu | Ser | Val | Glu | Ile | Tyr |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Asp | Lys | Phe | Gln | Arg | Ala | Thr | Ser | Ile | Lys | Arg | Lys | Leu | Ser | Ala | Glu |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Leu | Ala | Gly | Asn | His | Asn | Gln | Glu | Leu | Thr | Pro | Cys | Arg | Arg | Thr | Leu |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ser | Val | Asn | His | Leu | Thr | Ser | Glu | Arg | Asp | Val | Leu | Pro | Pro | Leu | Leu |
| | 385 | | | | 390 | | | | | 395 | | | | | 400 |
| Lys | Thr | Glu | Ser | Ile | Tyr | Leu | Asn | Gly | Leu | Ala | Pro | His | Cys | Ala | Gly |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Glu | Glu | Ile | Ala | Val | Ile | Glu | Asn | Ile | Lys | | | | | | |
| | | | 420 | | | | | 425 | | | | | | | |

<210> 46
 <211> 2130
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (35)
 <223> N AT POSITION 35 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2057)
 <223> N AT POSITION 2057 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2067)
 <223> N AT POSITION 2067 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2111)
 <223> N AT POSITION 2111 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2120)
 <223> N AT POSITION 2120 INDICATES UNDETERMINED
 NUCLEOTIDE

<400> 46
 ccataccta acgactcact atagggtctg agcgnccgcc cgggcagtaa aatgcctgcc 60
 cgtgcagctc ggagcgcgca gcccgctctt gaataagaag tgagtacaat ggcgtgtttg 120
 taaaaaaaaa cttcaagtcc gtctttttca aaaaacattt tgaatgctgc atgcctcatg 180
 cttcccagcg cctcgcggga gagaccggc tatagagcag gagtggcggc acctgacttg 240
 ctggatccta aatctgccgc tcagaactcc aaaccgaggc tctcattttc cacgaaaccc 300
 acagtgtctg cttcccgggt ggagagtgac acgaccatta atgttatgaa atggaagacg 360
 gtctccacga tattccttgg ggttgcctc tatctgatca tcggagccac cgtgttcaaa 420
 gcattggagc agcctcatga gatttcacag aggaccacca ttgtgatcca gaagcaaaaca 480
 ttcataatccc aacattcctg tgtcaattcg acggagctgg atgaactcat tcagcaaata 540
 gtggcagcaa taaatgcagg gattataccg ttaggaaaca cctccaatca aatcagtcac 600
 tgggatttgg gaagtccctt cttctttgct ggcactgtta ttacaacatc aggatttgga 660
 aacatctcac cacgcacaga aggcggcaaa atattctgta tcatctatgc cttactggga 720
 attcccctct ttggttttct cttggctgga gttggagatc agctaggcac catatttgga 780
 aaaggaattg ccaaagtggg agatacgttt attaagtggg atgttagtca gaccaagatt 840
 cgcatactct caacaatcat atttatacta tttggctgtg tactctttgt ggctctgcct 900
 gcgatcatat tcaaacacat agaaggctgg agtgccctgg acgccattta ttttgtggtt 960
 atcactctaa caactatttg atttgggtgac tacgttgtag gtggatccga tattgaatat 1020
 ctggacttct ataagcctgt cgtgtggttc tggatccttg tagggcttgc ttactttgct 1080
 gctgtcctga gcatgattgg gagattggct cgagtgatat ctaaaaagac aaaagaagag 1140
 gtgggagagt tcagagcaca cgctgctgag tggacagcca acgtcacagc cgaattcaaa 1200
 gaaaccagga ggcgactgag tgtggagatt tatgacaagt tccagcgggc cacctccatc 1260
 aagcgggaagc tctcggcaga actggctgga aaccacaatc aggagctgac tccttgtagg 1320
 aggaccctgt cagtgaacca cctgaccagc gagagggatg tcttgccctc cttactgaag 1380
 actgagagta tctatctgaa tggtttggtg ccacactgtg ctggtgaaga gattgctgtg 1440
 attgagaaca tcaaatagcc ctctctttaa ataacccttag gcatagccat aggtgaggac 1500
 ttctctatgc tctttatgac tgttgctggt agcatttttt aaattgtgca tgagctcaaa 1560
 gggggaacaa aatagataca cccatcatgg tcatctatca tcaagagaat ttggaattct 1620
 gagccagcac tttctttctg atgatgcttg ttgaacggcc cactttcttt gatgagtggg 1680
 atgacaagca atgtctgatg cttttgtgtg cccagactgt tttcctctct ctttccttaa 1740
 tgtgccataa ggcctcagaa tgaattgaga attgtttctg gtaacaatgt agctttgagg 1800
 gatcagttct taacttttca gggctctacct aactgagcct agatatggac catttatgga 1860
 tgacaacaat tttttttttg taaatgacaa gaaattctta tgcagccttt tacctaagaa 1920
 atttctgtca gtgccttatc ttatgaagaa acagaacctc tctagctaat gtgtgggtttc 1980
 tccttccctg cccccacccc taggctcacc tctgcagtct tttacccag ttctccatt 2040
 tgaataccat accttgntgg aaacagngtg taaaatgact gaagtgatga tgccgaagat 2100
 gaaatagatg ncaaattagn tggacattga 2130

<210> 47
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 47
 aaaagatcta aaatgcttcc cagcgcc

27

<210> 48
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 48
 aaagtcgacc tatttgatgt tctcaat

27

<210> 49
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 49
 aaaaagctta aaatgcttcc cagcgcc

27

<210> 50
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 50
 aaatctagac tatttgatgt tctcaat

27

<210> 51
 <211> 534
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (262)
 <223> N AT POSITION 262 INDICATES UNDETERMINED
 NUCLEOTIDE

<400> 51
 aacaaaaacc ttttttgttt tgaatggcct agagagggta agggatcccc tgacgaacag 60
 gagcagagcc agctagaacc tgggcctggc cagttcaagg ccaccagagg gcagccttct 120
 gcggaaggca gtattgggggt aggcagggac cccagcagac atggcactca gagctctcac 180
 tgtccactga ctctctcttc tccaggttat ggccacatgg cccactatc gccaggcgga 240
 aaggccttct gcatgggtctt antagccctt gggctgccag cctccttagc tctcgtggcc 300
 accctgcgcc attgcctgct gcctgtgctc agccgcccac gtgcctgggt agcgggtccac 360
 tggcagctgt caccggccag ggctgcgctg ctgcaggcag ttgactggg actgctgggtg 420
 gccagcagct ttgtgctgct gccagcgctg gtgctgtggg gccttcaggg cgactgcagc 480
 ctgctggggg ccgtctactt ctgcttcagc tcgctcagca ccattggcct gggg 534

<210> 52
 <211> 956
 <212> DNA

<213> Mus musculus

<400> 52

| | | | | | | |
|-------------|-------------|------------|------------|-------------|------------|-----|
| atgatacgat | ttaatacgac | tcactatagg | gaatttggcc | ctcgaggcca | agaattcggc | 60 |
| acgaggagaa | tgtgcgcacg | ttggctctca | tcgtgtgcac | cttcacctac | ctgctggtgg | 120 |
| gcgccgcggt | gttcgacgca | ctggagtcgg | agccggagat | gatcgagcgg | cagcggctgg | 180 |
| agctgcggca | gctggagctg | cgggcgcgct | acaacctcag | cgagggcggc | tacgaggagc | 240 |
| tggagcgcgt | cgtgctgcgc | ctcaagccgc | acaaggccgg | cgtgcagtgg | cgcttcgcgg | 300 |
| gctccttcta | cttcgccatc | accgtcatca | ccaccatcgg | ctatgggtcat | gcggcgccca | 360 |
| gcacggacgg | aggcaagggtg | ttctgcatgt | tctacgcgct | gctgggcatc | ccgctcacac | 420 |
| tagtcatggt | ccagagcctg | ggtgaacgca | tcaacacctc | cgtgaggtag | ctgctgcacc | 480 |
| gtgccaaagag | ggggctgggc | atgcggcacg | ccgaagtgtc | catggccaac | atggtgctca | 540 |
| tcggtttctgt | gtcgtgcac | agcacgctgt | gcacgcggcg | agctgccttc | tcctactacg | 600 |
| agcgtcggac | tttcttccag | gcctattact | actgcttcat | caccctcacc | accatcggct | 660 |
| tcggcgacta | tgtggcgctg | cagaaggacc | aggcgctgca | gacgcagccg | cagtatgtgg | 720 |
| cttcagcttc | gtgtacatcc | tcacgggctc | acggtcacgc | gcgcttcctc | aacctcgtgg | 780 |
| tgctgcgatt | catgaccatg | aacgccgagg | acgagaagcg | tgatgcggag | caccgcgccc | 840 |
| tgctcacgca | caacggccag | gctgtcggcc | tgggtggcct | gagctgcctg | agcggtagcc | 900 |
| tgggcgacgg | cgtgcgtccc | cgcgaccagg | tcacatgcgc | tgcggccgca | agctta | 956 |

<210> 53

<211> 1055

<212> DNA

<213> Mus musculus

<220>

<221> unsure

<222> (247)

<223> N AT POSITION 247 INDICATES UNDETERMINED NUCLEOTIDE

<220>

<221> unsure

<222> (593)

<223> N AT POSITION 593 INDICATES UNDETERMINED NUCLEOTIDE

<220>

<221> unsure

<222> (952)

<223> N AT POSITION 952 INDICATES UNDETERMINED NUCLEOTIDE

<400> 53

| | | | | | | |
|------------|-------------|-------------|-------------|------------|-------------|------|
| ctgaaaccat | gggcccagata | cctgctcctg | cttatggccc | acctgctggc | catgggcctt | 60 |
| ggggctgtgg | tgcttcaggc | cctggagggc | cctccagctc | gccacctcca | ggcccagggtc | 120 |
| caggctgaac | tggctagctt | ccaggcagag | cacagggcct | gcttgccacc | tgaggccctg | 180 |
| gaggagctgc | taggtgcggg | cctgagagca | caggcccatg | gagtttccag | cctgggcaac | 240 |
| agctcanaga | caagcaactg | ggatctgccc | tcagctctgc | tgttcactgc | cagcatcctc | 300 |
| accaccaccg | gttatggcca | catggcccca | ctctcctcag | gtggaaaagg | cttctgtgtg | 360 |
| gtctatgcag | cccttgggct | gccagcctct | ctagcacttg | tggtgcctct | gcgccactgc | 420 |
| ttgctgcctg | tgttcagctg | cccagggtgac | tgggtagcca | ttcgctggca | gctggcacca | 480 |
| gctcaggctg | ctctgctaca | ggcagcagga | ctgggcctcc | tggtggcctg | tgtcttcatg | 540 |
| ctgtctccag | cactgggtgct | gtgggggtgta | caggggtgact | ggcagcctgc | tanaaccatc | 600 |
| tacttctgtt | tcggctcact | cagcacgata | ggcctaggag | acttgctgcc | tgcccattgga | 660 |
| cgtggcctgc | accagcccat | ttaccacctt | gggcagtttg | cacttcttgg | ttacttgctc | 720 |
| ctggggctcc | tggccatggt | gttagcagta | gagaccttct | cagagctgcc | tcagggtccgt | 780 |
| gccatggtga | aattcttttg | gcccagtggc | tctagaaccg | atgaagatca | agatggcatc | 840 |
| ctaggccaag | atgagctggc | tctgagcact | gtgctgcctg | acgccccagt | cttgggacca | 900 |
| accacccag | cctgagcggg | aggcaccaag | gagtgcttga | agaacatagc | angaagggtt | 960 |
| atgggaatga | atatgtcatg | ggataatggt | aattttaaaa | attaaatggg | ctgcttagca | 1020 |
| tgcaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | aaaaa | | | 1055 |

<210> 54
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (88)
 <223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 54
 Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
 1 5 10 15
 Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
 20 25 30
 Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
 35 40 45
 Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
 50 55 60
 Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
 65 70 75 80
 Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
 85 90 95
 Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
 100 105 110
 Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
 115 120 125
 Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
 130 135 140
 Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
 145 150 155 160
 Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
 165 170 175
 Leu Gly

<210> 55
 <211> 309
 <212> PRT
 <213> Mus musculus

<400> 55
 Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
 1 5 10 15
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
 20 25 30
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln

35 40 45
 Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
 50 55 60
 Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
 65 70 75 80
 His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
 85 90 95
 Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
 100 105 110
 Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
 115 120 125
 Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
 130 135 140
 Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
 145 150 155 160
 Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
 165 170 175
 Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
 180 185 190
 Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
 195 200 205
 Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
 210 215 220
 Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala
 225 230 235 240
 His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255
 Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270
 Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285
 Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
 290 295 300
 Ala Ala Ala Ser Leu
 305

<210> 56

<211> 304

<212> PRT

<213> Mus musculus

<220>

<221> UNSURE

<222> (83)

<223> N AT POSITION 83 INDICATES UNDETERMINED RESIDUE

<220>

<221> UNSURE

<222> (198)

<223> N AT POSITION 198 INDICATES UNDETERMINED RESIDUE

<400> 56

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Lys | Pro | Trp | Ala | Arg | Tyr | Leu | Leu | Leu | Leu | Met | Ala | His | Leu | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ala | Met | Gly | Leu | Gly | Ala | Val | Val | Leu | Gln | Ala | Leu | Glu | Gly | Pro | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Arg | His | Leu | Gln | Ala | Gln | Val | Gln | Ala | Glu | Leu | Ala | Ser | Phe | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Glu | His | Arg | Ala | Cys | Leu | Pro | Pro | Glu | Ala | Leu | Glu | Glu | Leu | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Ala | Val | Leu | Arg | Ala | Gln | Ala | His | Gly | Val | Ser | Ser | Leu | Gly | Asn |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 |
| Ser | Ser | Xaa | Thr | Ser | Asn | Trp | Asp | Leu | Pro | Ser | Ala | Leu | Leu | Phe | Thr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | Ser | Ile | Leu | Thr | Thr | Thr | Gly | Tyr | Gly | His | Met | Ala | Pro | Leu | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Gly | Gly | Lys | Ala | Phe | Cys | Val | Val | Tyr | Ala | Ala | Leu | Gly | Leu | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Ser | Leu | Ala | Leu | Val | Ala | Ala | Leu | Arg | His | Cys | Leu | Leu | Pro | Val |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Phe | Ser | Arg | Pro | Gly | Asp | Trp | Val | Ala | Ile | Arg | Trp | Gln | Leu | Ala | Pro |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ala | Gln | Ala | Ala | Leu | Leu | Gln | Ala | Ala | Gly | Leu | Gly | Leu | Leu | Val | Ala |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Cys | Val | Phe | Met | Leu | Leu | Pro | Ala | Leu | Val | Leu | Trp | Gly | Val | Gln | Gly |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Asp | Trp | Gln | Pro | Ala | Xaa | Thr | Ile | Tyr | Phe | Cys | Phe | Gly | Ser | Leu | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Ile | Gly | Leu | Gly | Asp | Leu | Leu | Pro | Ala | His | Gly | Arg | Gly | Leu | His |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Pro | Ala | Ile | Tyr | His | Leu | Gly | Gln | Phe | Ala | Leu | Leu | Gly | Tyr | Leu | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Gly | Leu | Leu | Ala | Met | Leu | Leu | Ala | Val | Glu | Thr | Phe | Ser | Glu | Leu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Pro | Gln | Val | Arg | Ala | Met | Val | Lys | Phe | Phe | Gly | Pro | Ser | Gly | Ser | Arg |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Thr | Asp | Glu | Asp | Gln | Asp | Gly | Ile | Leu | Gly | Gln | Asp | Glu | Leu | Ala | Leu |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Ser | Thr | Val | Leu | Pro | Asp | Ala | Pro | Val | Leu | Gly | Pro | Thr | Thr | Pro | Ala |
| | 290 | | | | | 295 | | | | | 300 | | | | |

<210> 57

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (1)..(9)

<223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT
POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8
IS Y, F, V, I, M, OR L

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<400> 57

Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
1 5

<210> 58

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(8)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I,
V, L, F, OR Y

<400> 58

Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa
1 5

<210> 59

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<400> 59

Tyr Ala Leu Leu Gly Ile Pro
1 5

<210> 60

<211> 7

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: POTASSIUM ION
 CHANNEL SEQUENCE

<220>
 <221> VARIANT
 <222> (6)
 <223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60
 Tyr Ala Leu Leu Gly Xaa Pro
 1 5

<210> 61
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (88)
 <223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61
 Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
 1 5 10 15
 Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
 20 25 30
 Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
 35 40 45
 Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
 50 55 60
 Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
 65 70 75 80
 Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
 85 90 95
 Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
 100 105 110
 Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
 115 120 125
 Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
 130 135 140
 Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
 145 150 155 160
 Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
 165 170 175
 Leu Gly

<210> 62
 <211> 309
 <212> PRT
 <213> Mus musculus

<400> 62
 Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
 1 5 10 15
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
 20 25 30
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
 35 40 45
 Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
 50 55 60
 Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
 65 70 75 80
 His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
 85 90 95
 Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
 100 105 110
 Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
 115 120 125
 Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
 130 135 140
 Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
 145 150 155 160
 Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
 165 170 175
 Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
 180 185 190
 Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
 195 200 205
 Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
 210 215 220
 Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala
 225 230 235 240
 His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255
 Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270
 Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285
 Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
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290

295

Ala Ala Ala Ser Leu
305

<210> 63
<211> 434
<212> PRT
<213> Caenorhabditis elegans

<400> 63
Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala
1 5 10 15
Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val
20 25 30
Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro
35 40 45
Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp
50 55 60
Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro
65 70 75 80
Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro
85 90 95
Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu
100 105 110
Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser
115 120 125
Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn
130 135 140
Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp
145 150 155 160
Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys
165 170 175
Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn
180 185 190
Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val
195 200 205
Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp
210 215 220
Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala
225 230 235 240
Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn
245 250 255
Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu
260 265 270

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Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly
 275 280 285
 Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu
 290 295 300
~~Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val~~
~~305 310 315 320~~
 Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile
 325 330 335
 Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Phe Cys Asn Tyr Arg
 340 345 350
 Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe
 355 360 365
 Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala
 370 375 380
 Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg
 385 390 395 400
 Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr
 405 410 415
 Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser
 420 425 430
 Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
 CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
 S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,
 L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro
 1 5

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
 sequence between Ce orf1 and Dm orf1

<400> 65
Thr Trp Thr Phe
1

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

<400> 66
Gly Tyr Gly Asn
1

<210> 67
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

<400> 67
Gly Phe Gly Asp
1